

Figure 1A

1 CACCAGCAGTAGTAGCAGAAGCGAAGAGCGCAAACGCAACCGCTCTCCCCGCGCGTTGGC 60

61 CGATTCATTAATGCAGCTGGCACGACAGGTTTCCCGACTGGAAAGCGGGCAGTGAGCGCA 120

121 ACGCAATTAATGTGAGTTAGCTCACTCATTAGGCACCCCAGGCTTTACACTTTATGCTTC 180

181 CGGCTCGTATGTTGTGTGGAATTGTGAGCGGATAACAATTTACACAGGAAACAGCTATG 240

241 ACCATGATTACGCCAAGCTCGAAATTAACCCCTCACTAAAGGGAACAAAAGCTGGAGCTCC 300

301 ACCGCGGTGGCGGCCGCTCTAGAACTAGTGGATCCCCCGGGCTGCAGGAATTCGGCACGA 360

361 GAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCAT 420  
1 M 1

421 GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATCATTATTCTGGCTGG 480  
2 A S L G Q I L F W S I I S I I I I L A G 21

481 AGCAATTGCACTCATCATTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTAC 540  
22 A I A L I I G F G I S G R H S I T V T T 41

541 TGTCGCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGA 600  
42 V A S A G N I G E D G I L S C T F E P D 61

601 CATCAAACCTTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCA 660  
62 I K L S D I V I Q W L K E G V L G L V H 81

661 TGAGTTCAAAGAAGGCAAAGATGAGCTGTGCGGAGCAGGATGAAATGTTTCAGAGCCCGGAC 720  
82 E F K E G K D E L S E Q D E M F R G R T 101

721 AGCAGTGTTTGCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCA 780  
102 A V F A D Q V I V G N A S L R L K N V Q 121

781 ACTCACAGATGCTGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGC 840  
122 L T D A G T Y K C Y I I T S K G K G N A 141

841 TAACCTTGAGTATAAACTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGC 900  
142 N L E Y K T G A F S M P E V N V D Y N A 161

901 CAGCTCAGAGACCTTGCGGTGTGAGGCTCCCCGATGGTTCCCCCAGCCCACAGTGGTCTG 960  
162 S S E T L R C E A P R W F P Q P T V V W 181

961 GGCATCCCAGTTGACCAGGAGCCAACCTTCTCGGAAGTCTCCAATACCAGCTTTGAGCT 1020  
182 A S Q V D Q G A N F S E V S N T S F E L 201

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Figure 1B

1021	GAAGCTCTGAGAATGTGACCATGAAGGTTGTGTCTGTGCTCTACAATGTTACGATCAACAA	1080
202	N S E N V T M K V V S V L Y N V T I N N	221
1081	CACATACTCCTGTATGATTGAAAATGACATTGCCAAAGCAACAGGGGATATCAAAGTGAC	1140
222	T Y S C M I E N D I A K A T G D I K V T	241
1141	AGAATCGGAGATCAAAAGGCGGAGTCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTG	1200
242	E S E I K R R S H L Q L L N S K A S L C	261
1201	TGTCTCTTCTTTCTTTGCCATCAGCTGGGCACTTCTGCCTCTCAGCCCTTACCTGATGCT	1260
262	V S S F F A I S W A L L P L S P Y L M L	281
1261	AAAATAATGTGCCTTGGCCACAAAAAGCATGCAAAGTCATTGTTACAACAGGGATCTAC	1320
282	K *	283
1321	AGAACTATTTCACCACCAGATATGACCTAGTTTATATTCTGGGAGGAAATGAATTCAT	1380
1381	ATCTAGAAGTCTGGAGTGAGCAACAAGAGCAAGAAACAAAAGAAGCCAAAAGCAGAAG	1440
1441	GCTCCAATATGAACAAGATAAAATCTATCTTCAAAGACATATTAGAAGTTGGGAAAATAAT	1500
1501	TCATGTGAAGTAGACAAGTGTGTTAAGAGTGATAAGTAAATGCACGTGGAGACAAGTGC	1560
1561	ATCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCTGGGGAGTGAGAGGACAGGATAG	1620
1621	TGCATGTTCTTTGTCTCTGAATTTTTAGTTATATGTGCTGTAATGTTGCTCTGAGGAAGC	1680
1681	CCCTGGAAAGTCTATCCCAACATATCCACATCTTATATCCACAAATTAAGCTGTAGTAT	1740
1741	GTACCCTAAGACGCTGCTAATCGACTGCCACTTCGCAACTCAGGGGCGGCTGCATTTTAG	1800
1801	TAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAAGGTGCCTTGCTTCTCTTCCC	1860
1861	AACTGACAAATGCCAAAGTTGAGAAAAATGATCATAATTTAGCATAAACAGAGCAGTCG	1920
1921	GCGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAACAAATGCGGGTTT	1980
1981	ATTTCTCAGATGATGTTTCATCCGTGAATGGTCCAGGGAAGGACCTTTCACCTTGACTATA	2040
2041	TGGCATTATGTCATCACAAGCTCTGAGGCTTCTCCTTTCCATCCTGCGTGGACAGCTAAG	2100
2101	ACCTCAGTTTTCATAGCATCTAGAGCAGTGGGACTCAGCTGGGGTGATTTGCCCCCCA	2160
2161	TCTCCGGGGGAATGTCTGAAGACAATTTTGGTTACCTCAATGAGGGAGTGAGGAGGATA	2220

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Figure 1C

2221 CAGTGCTACTACCAACTAGTGGATAAAGGCCAGGGATGCTGCTCAACCTCCTACCATGTA 2280  
2281 CAGGACGTCTCCCCATTACAAC TACCCAATCCGAAGTGTCAACTGTGTCAGGACTAAGAA 2340  
2341 ACCCTGGTTTTTGAGTAGAAAAGGGCCTGGAAAGAGGGGAGCCAACAAATCTGTCTGCTTC 2400  
2401 CTCACATTAGTCATTGGCAAATAAGCATTCTGTCTCTTTGGCTGCTGCCTCAGCACAGAG 2460  
2461 AGCCAGAACTCTATCGGGCACCAGGATAACATCTCTCAGTGAACAGAGTTGACAAGGCCT 2520  
2521 ATGGGAAATGCCTGATGGGATTATCTTCAGCTTGTTGAGCTTCTAAGTTTCTTTCCCTTC 2580  
2581 ATTCTACCTGCAAGCCAAGTTCTGTAAGAGAAATGCCTGAGTCTAGCTCAGGTTTTCT 2640  
2641 TACTCTGAATTTAGATCTCCAGACCCTTCCTGGCCACAATTCAAATTAAGGCAACAAACA 2700  
2701 TATACCTTCATGAAGCACACAGACTTTTGAAAGCAAGGACAATGACTGCTTGAATTG 2760  
2761 AGGCCTTGAGGAATGAAGCTTTGAAGGAAAAGAATACTTTGTTTCCAGCCCCCTTCCCAC 2820  
2821 ACTCTTCATGTGTTAACCCTGCCTTCCTGGACCTTGGAGCCACGGTGACTGTATTACAT 2880  
2881 GTTGTTATAGAAAAC T GATTTTAGAGTCTGATCGTTCAAGAGAATGATTAAATATACAT 2940  
2941 TTCCTAAAAAAAAAAAAAAAAAACTCGAGGGGGGGCCCGGTACCCAATTCGCCCTATAGT 3000  
3001 GAGTCGTATTACAATTCACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAACCTGGC 3060  
3061 GTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTTCGCCAGCTGGCGTAATAGCGAA 3120  
3121 GAGGCCCGCACCGATCGCCCTTCCCAACA KTTGCGCAGCCTGAATGGCGAATGGCAAATT 3180  
3181 GTAAGCGTTAATATTTTGT TAAATTCGCGTTAAATTTTGT TAAATCAGCTCATTTTTT 3240  
3241 AACCAATAGGCCGAAATCGGC AAAATCCCTTATAAATCAAAGAATAGACCGAGATAGGG 3300  
3301 TTGAGTGTGTTCCAGTTTGG AACAAGAGTCCACTATTAAAGTGTTCACCGCGGTGA 3357

Figure 2

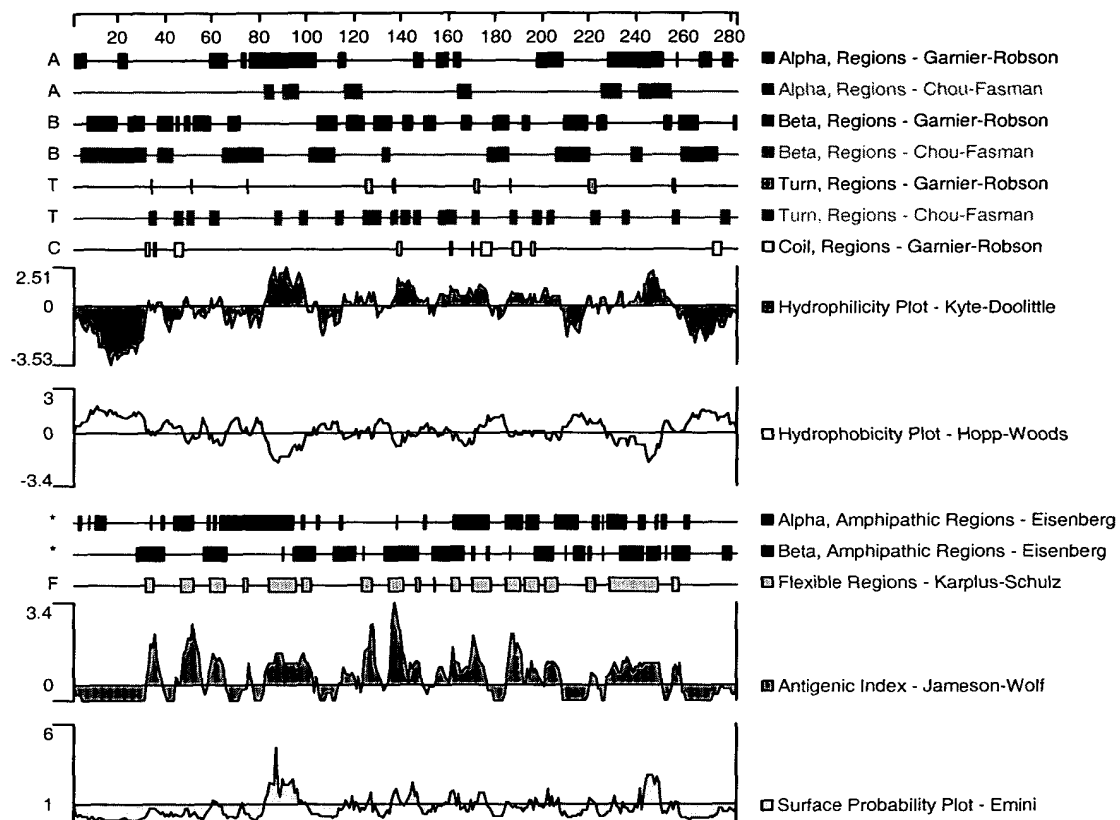


Figure 3A

1 CCACGCGTCCGGAATGAACAACCTTTCTCTCTTGAATATATCTTAACGCCAAATTTTGA 60  
61 GTGCTTTTTTGTACCCATCCTCATATGTCCCAGCTGGAAAGAATCCTGGGTGGAGCTA 120  
121 CTGCATGTTGATTGTTTTGTTTTTCCTTTTGGCTGTTCATTTTGGTGGCTACTATAAGGA 180  
181 AATCTAACACAAACAGCAACTGTTTTTTGTTGTTTACTTTTGCATCTTTACTTGTGGAGC 240  
241 TGTGGCAAGTCCTCATATCAAATACAGAACATGATCTTCCTCCTGCTAATGTTGAGCCTG 300  
1 M I F L L L M L S L 10  
301 GAATTGCAGCTTCACCAGATAGCAGCTTTATTACAGTGACAGTCCCTAAGGAACGTGAC 360  
11 E L Q L H Q I A A L F T V T V P K E L Y 30  
361 ATAATAGAGCATGGCAGCAATGTGACCCTGGAATGCAACTTTGACACTGGAAGTCATGTG 420  
31 I I E H G S N V T L E C N F D T G S H V 50  
421 AACCTTGGAGCAATAACAGCCAGTTTGCAAAAGGTGGAAAATGATACATCCCCACACCGT 480  
51 N L G A I T A S L Q K V E N D T S P H R 70  
481 GAAAGAGCCACTTTGCTGGAGGAGCAGCTGCCCTAGGGAAGGCCTCGTTCACATACCT 540  
71 E R A T L L E E Q L P L G K A S F H I P 90  
541 CAAGTCCAAGTGAGGGACGAAGGACAGTACCAATGCATAATCATCTATGGGGTCGCCTGG 600  
91 Q V Q V R D E G Q Y Q C I I I Y G V A W 110  
601 GACTACAAGTACCTGACTCTGAAAGTCAAAGCTTCCTACAGGAAAATAAACACTCACATC 660  
111 D Y K Y L T L K V K A S Y R K I N T H I 130  
661 CTAAAGGTTCCAGAAACAGATGAGGTAGAGCTCACCTGCCAGGCTACAGGTTATCCTCTG 720  
131 L K V P E T D E V E L T C Q A T G Y P L 150  
721 GCAGAAGTATCCTGGCCAAACGTCAGCGTTCTGCCAACACCAGCCACTCCAGGACCCCT 780  
151 A E V S W P N V S V P A N T S H S R T P 170  
781 GAAGGCCTCTACCAGGTCACCAGTGTCTGCGCCTAAAGCCACCCCCTGGCAGAAACTTC 840  
171 E G L Y Q V T S V L R L K P P P G R N F 190  
841 AGCTGTGTGTCTGGAATACTCACGTGAGGGAACCTACTTTGGCCAGCATTGACCTTCAA 900  
191 S C V F W N T H V R E L T L A S I D L Q 210  
901 AGTCAGATGGAACCCAGGACCCATCCAACCTGGCTGCTTCACATTTTCATCCCCCTCCTGC 960  
211 S Q M E P R T H P T W L L H I F I P S C 230  
961 ATCATTGCTTTTCATTTTCATAGCCACAGTGATAGCCCTAAGAAAACAACTCTGTCAAAG 1020  
231 I I A F I F I A T V I A L R K Q L C Q K 250

Figure 3B

1021 CTGTATTCTTCAAAGACACAACAAAAGACCTGTCACCACAACAAAGAGGAAGTGAAC 1080  
251 L Y S S K D T T K R P V T T T K R E V N 270

1081 AGTGCTGTGAATCTGAACCTGTGGTCTTGGGAGCCAGGGTGACCTGATATGACATCTAAA 1140  
271 S A V N L N L W S W E P G \* 284

1141 GAAGCTTCTGGACTCTGAACAAGAATTCGGTGGCCTGCAGAGCTTGCCATTTGCACTTTT 1200

1201 CAAATGCCCTTTGGATGACCCAGCACTTTAATCTGAAACCTGCAACAAGACTAGCCAACAC 1260

1261 CTGGCCATGAAACTTGCCCCCTTCACTGATCTGGACTCACCTCTGGAGCCTATGGCTTTAA 1320

1321 GCAAGCACTACTGCACTTTACAGAATTACCCCACTGGATCCTGGACCCACAGAATTCCTT 1380

1381 CAGGATCCTTCTTGCTGCCAGACTGAAAGCAAAAGGAATTATTTCCCTCAAGTTTCTA 1440

1441 AGTGATTTCAAAAGCAGAGGTGTGTGGAATTTCCAGTAACAGAAACAGATGGGTGACC 1500

1501 AATAGAGTTATTTTTTATCTATAGCTTCCTCTGGGTACTAGAAGAGGCTATTGAGACTAT 1560

1561 GAGCTCACAGACAGGGCTTCGCACAAACTCAAATCATAATTGACATGTTTTATGGATTAC 1620

1621 TGGAATCTTGATAGCATAATGAAGTTGTCTAATTAACAGAGAGCATTTAAATATACACT 1680

1681 AAGTGACAAAATTGTGGAGTAAAGTCATCAAGCTCTGTTTTTGAGGTCTAAGTCACAAAG 1740

1741 CATTTGTTTTAACCTGTAATGGCACCATGTTTAATGGTGGTTTTTTTTTTGAAGTACATC 1800

1801 TTTCTTTAAAAATTATTGGTTTCTTTTTATTGTTTTTACCTTAGAAATCAATTATATA 1860

1861 CAGTCAAAAATATTGATATGCTCATACGTTGTATCTGCAGCAATTCAGATAAGTAGCT 1920

1921 AAAATGGCCAAAGCCCCAAACTAAGCCTCCTTTTCTGGCCCTCAATATGACTTTAAATTT 1980

1981 GACTTTTCAGTGCCTCAGTTTGACATCTGTAATACAGCAATGCTAAGTAGCAAGGCCT 2040

2041 TTGATAATTGGCACTATGGAAATCCTGCAAGATCCCACTACATATGTGTGGAGCAGAAGG 2100

2101 GTAACTCGGCTACAGTAACAGCTTAATTTGTGTTAAATTTGTTCTTTATACTGGAGCCATG 2160

2161 AAGCTCAGAGCATTAGCTGACCCTTGAACATTCAAATGGGCACATTAGCTAGTATAACA 2220

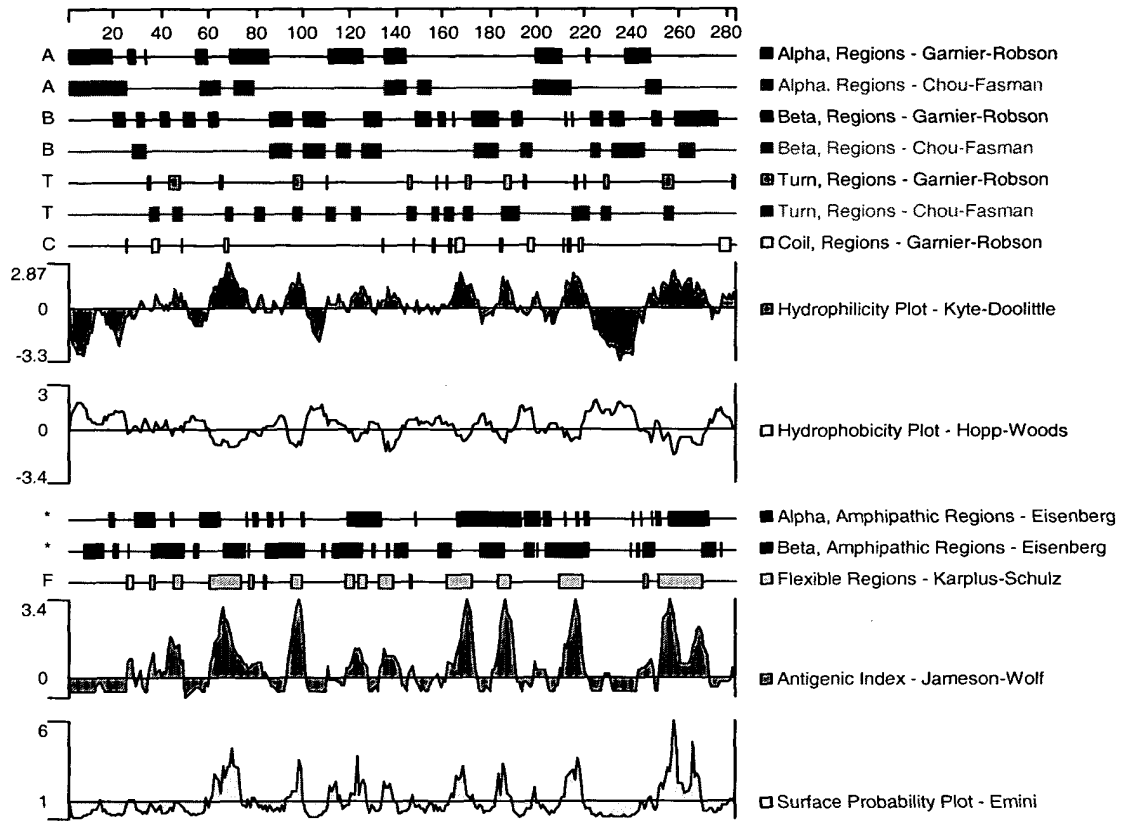
2221 GACTTACATAGGTGGGCCATAAGCAAGCTCCTTAAGTGAAGCAAAATTTGGGGCTTATGAG 2280

**Figure 3C**

2281 AATGAAAGGGTGTGAAATTGACTAACAGACAAATCATACATCTCAGTTTCTCAATTCTCA 2340  
2341 TGTAAATCAGAGAATGCCTTTAAAGAATAAACTCAATTGTTATTCTTCAAAAAAAAAA 2400  
2401 AAAAAA 2406

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Figure 4



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Figure 5A

1 GGCACGAGCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCCATGGCT 60  
1 M A 2  
61 CTCATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT 120  
3 L M L S L V L S L L K L G S G Q W Q V F 22  
121 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGGAGGACGACGAGCATTCTCCTGTTTCCTG 180  
23 G P D K P V Q A L V G E D A A F S C F L 42  
181 TCTCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGTTCTTTCAGGGGCCAGTTCTCTAGC 240  
43 S P K T N A E A M E V R F F R G Q F S S 62  
241 GTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAA 300  
63 V V H L Y R D G K D Q P F M Q M P Q Y Q 82  
301 GGCAGGACAAAAGTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGGAA 360  
83 G R T K L V K D S I A E G R I S L R L E 102  
361 AACATTACTGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTAC 420  
103 N I T V L D A G L Y G C R I S S Q S Y Y 122  
421 CAGAAGGCCATCTGGGAGCTACAGGTGTGCACTGGGCTCAGTTCCTCTCATTTCCATC 480  
123 Q K A I W E L Q V S A L G S V P L I S I 142  
481 GCGGGATATGTTGATAGAGACATCCAGCTACTCTGTGTCAGTCCCTCGGGCTGGTTCCCCCGG 540  
143 A G Y V D R D I Q L L C Q S S G W F P R 162  
541 CCCACAGCGAAGTGGAAAGGTCCACAAGGACAGGATTTGTCCACAGACTCCAGGACAAAC 600  
163 P T A K W K G P Q G Q D L S T D S R T N 182  
601 AGAGACATGCATGGCCTGTTTGATGTGGAGATCTCTCTGACCGTCCAAGAGAACGCCGGG 660  
183 R D M H G L F D V E I S L T V Q E N A G 202  
661 AGCATATCCTGTTCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAG 720  
203 S I S C S M R H A H L S R E V E S R V Q 222  
721 ATAGGAGACTGGAGAAGAAAGCACGGACAGGCAGGTAAAAGAAAATATTCCTCTTCACAC 780  
223 I G D W R R K H G Q A G K R K Y S S S H 242  
781 ATTTATGACTCCTTTCCAAGTCTCTCGTTTATGGATTTTATATCCTGAGGCCCGTGGGT 840  
243 I Y D S F P S L S F M D F Y I L R P V G 262  
841 CCCTGCAGAGCCAAGCTTGTGATGGGAAGTCTGAAATTGCAGATTCTGGGGGAGGTGCAT 900  
263 P C R A K L V M G T L K L Q I L G E V H 282  
901 TTTGTAGAGAAGCCCCATAGCCTTCTTCAGATCTCTGGAGGGTCCACAACACTCAAAAAG 960  
283 F V E K P H S L L Q I S G G S T T L K K 302

**Figure 5B**

961 GGTCCCAATCCTTGGTCTTTCCCTTCTCCCTGCGCCCTGTTTCCCACGTGAGCACGGAAC 1020  
303 G P N P W S F P S P C A L F P T \* 319

1021 TGCCTGCTCTCTCTGCTTTCAGAAATTGAGAGACGCCCGGAAACACGCAGGTACCAA 1080

1081 CGCCTGAGAGGGTAACAGTGGGCATGGAGTAGGAAGATGACCAGTGACAGATATGGAGCC 1140

1141 CATCCAGCTTGTAGACAGCAAATCTGTGATGCCCCAATCCACCCAGGGTGCAGCTGCCT 1200

1201 CTAAATACACTTCTTGGCCCAGGACTTGGAGGGAAAAGCGTAGGACTGGGTCAGCTAGG 1260

1261 AGGGGTCACAGGCAAGACGCCAGGGAACAGGGCATTAGTAGCTGGCTTCAGGGGTCT 1320

1321 GTGCAAAGGGGAACGAAGTGAAGTTAGCAGGAACGGTGGGTGGAAGGAAGCTGAATCCT 1380

1381 GGAGTCACTCAAGGTCTCACAAAGTCAAATAGAGGGCTTACGTGGGAGGGCAGTGGTAGG 1440

1441 GCTGGGTGAACATCTCATGGTTGAGCATCTCCAAGCATCAGTGAGGCACGGGGGCTGCCC 1500

1501 TGGAGAAGGTACATGGCTGGTGGGATAGTGGGACTGGCCGGATCCTACCCGGAGCCAGTC 1560

1561 TGCAGTGGGAGGGTCGACCTCTTGCTCCAGCCCAGATTTCTGCTTCAGTAACTCATGCTT 1620

1621 CCTCTCTCCCCACCGCACCCCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGA 1680

1681 AGCTCTGCGTTTCTGATCTGAAACTGTAACCCATAGAAAAGCTCCTCAGGAGGTGCCTC 1740

1741 ACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGA 1800

1801 AACATTACTGGGAGGTGGACGTGGGACAAAATGTAGGGTGGTATGTGGGAGTGTGTCGGG 1860

1861 ATGACGTAGACAGGGGAAGAACAATGTGACTTTGTCTCCCAACAATGGGTATTGGGTCC 1920

1921 TCAGACTGACAACAGAACATTTGTATTTACATTCAATCCCCATTTTATCAGCCTCCCCC 1980

1981 CCAGCACCCCTCTACACGAGTAGGGGTCTTCTGGACTATGAGGGTGGGACCATCTCCT 2040

2041 TCTTCAATACAAATGACCAGTCCCTTATTTATACCCTGCTGACATGTCAGTTTGAAGGCT 2100

2101 TGTTGAGACCCTATATCCAGCATGCGATGTATGACGAGGAAAAGGGGACTCCCATATTCA 2160

2161 TATGTCCAGTGTCTGGGGATGAGACAGAGAAGACCCTGCTTAAAGGGCCCCACACCACA 2220

1000 900 800 700 600 500 400 300 200 100 0

**Figure 5C**

2221 GACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGCCCCAGCTTCCTCTCCGGAG 2280  
2281 CCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCCT 2340  
2341 GAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTG 2400  
2401 GGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGT 2460  
2461 TTGTGAAAAC TCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCCAGGCTCCTCA 2520  
2521 TTTGCTAGTCACGGACAGTGATTCTCTGCCCTCACAGGTGAAGATTAAAGAGACAACGAATG 2580  
2581 TGAATCATGCTTGCAGGTTT GAGGGCCACAGTGTTTGCTAATGGATGTGTTTTATGATT 2640  
2641 ATACATTTTCCCCACCATAAAACTCTGTTTGCCTTAATCCCACATTAATTAACTTTTC 2700  
2701 CTCCTATACCCAAATCCACCCATGGAATAGTTAATTGGAACACCTGCCTTTGTGAGGCTC 2760  
2761 CAAAGAATAAAGAGGAGGTAGGATTTTTCAC TGATTCTATAAGCCCAGCATTACCTGATA 2820  
2821 CCAAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAAC TACAGGTCCATATCCCTCA 2880  
2881 TTAACACAGACACAAAAATTCTAAATAAAATTTTAACAAAT TAAACTAAACAATATATTT 2940  
2941 AAAGATGATATATAACTACTCAGTGTGGTTTGTCCACAAATGCAGAGTTGGTTTAATAT 3000  
3001 TTAAATATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAAAAAAAAAAAAAAAAA 3059

2221 GACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGCCCCAGCTTCCTCTCCGGAG 2280  
2281 CCTGCGCACAGAGAGTCACGCCCCCACTCTCCTTTAGGGAGCTGAGGTTCTTCTGCCCT 2340  
2341 GAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGATTGGCCTGACCCTGTG 2400  
2401 GGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCACATTAGGTTTAGT 2460  
2461 TTGTGAAAAC TCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCCCAGGCTCCTCA 2520  
2521 TTTGCTAGTCACGGACAGTGATTCTCTGCCCTCACAGGTGAAGATTAAAGAGACAACGAATG 2580  
2581 TGAATCATGCTTGCAGGTTT GAGGGCCACAGTGTTTGCTAATGGATGTGTTTTATGATT 2640  
2641 ATACATTTTCCCCACCATAAAACTCTGTTTGCCTTAATCCCACATTAATTAACTTTTC 2700  
2701 CTCCTATACCCAAATCCACCCATGGAATAGTTAATTGGAACACCTGCCTTTGTGAGGCTC 2760  
2761 CAAAGAATAAAGAGGAGGTAGGATTTTTCAC TGATTCTATAAGCCCAGCATTACCTGATA 2820  
2821 CCAAAACCAGGCAAAGAAAACAGAAGAAGAGGAAGGAAAAC TACAGGTCCATATCCCTCA 2880  
2881 TTAACACAGACACAAAAATTCTAAATAAAATTTTAACAAAT TAAACTAAACAATATATTT 2940  
2941 AAAGATGATATATAACTACTCAGTGTGGTTTGTCCACAAATGCAGAGTTGGTTTAATAT 3000  
3001 TTAAATATCAACCAGTGTAATTCAGCACATTAATAAAGTAAAAAAAAAAAAAAAAAAAAA 3059

Figure 6

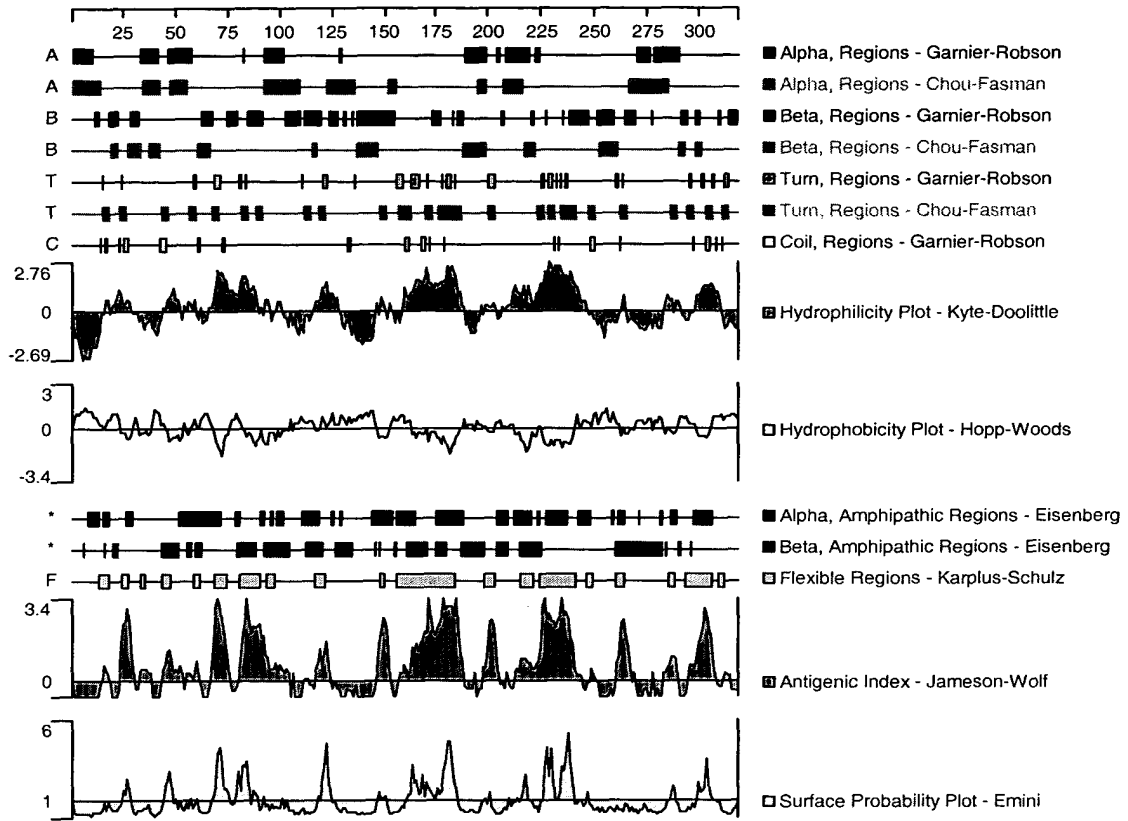


Figure 7A

1 NNCACGAGCCTGTGCCCTGGAAAGGTTGGAGACTTGGGGGACGACTGGAGAATTGCCAT 60  
61 TTGAGGACCAAAGGAGAAAAGAACTACACGCTAATTCTAGAGGCCTCCTGTCCCTGCC 120  
121 TGCTCTGGGTGCTCATGGAACCAGCTGCTGCCCTGCACTTCTCCCGCCAGCCTCCCTCC 180  
1 M E P A A A L H F S R P A S L L 16  
181 TCCTCCTCCTCAGCCTGTGTGCACTGGTCTCAGCCCAGTTTACTGTCGTGGGGCCAGCTA 240  
17 L L L S L C A L V S A Q F T V V G P A N 36  
241 ATCCCATCCTGGCCATGGTGGGAGAAAACACTACATTACGCTGCCATCTGTACCCCGAGA 300  
37 P I L A M V G E N T T L R C H L S P E K 56  
301 AAAATGCTGAGGACATGGAGGTGCGGTGGTTCCGGTCTCAGTTCTCCCCGCAGTGTTTG 360  
57 N A E D M E V R W F R S Q F S P A V F V 76  
361 TGTATAAGGTTGGGAGAGAGAGAACAGAGGAGCAGATGGAGGAGTACCGGGAAGAATCA 420  
77 Y K G G R E R T E E Q M E E Y R G R I T 96  
421 CCTTTGTGAGCAAAGACATCAACAGGGGCAGCGTGGCCCTGGTCATACATAACGTCACAG 480  
97 F V S K D I N R G S V A L V I H N V T A 116  
481 CCCAGGAGAATGGGATCTACCGCTGTCTTCCAAGAAGGCAGGTCCTACGATGAGGCCA 540  
117 Q E N G I Y R C Y F Q E G R S Y D E A I 136  
541 TCCTACGCCTCGTGGTGGCAGGCCTTGGGTCTAAGCCCCCTCATTGAAATCAAGGCCCAAG 600  
137 L R L V V A G L G S K P L I E I K A Q E 156  
601 AGGATGGGAGCATCTGGCTGGAGTGCATATCTGGAGGGTGGTACCCAGAGCCCCCTCACAG 660  
157 D G S I W L E C I S G G W Y P E P L T V 176  
661 TGTGGAGGGACCCCTACGGTGAGGTTGTGCCCCCCTGAAGGAGGTTTCCATCGCTGATG 720  
177 W R D P Y G E V V P A L K E V S I A D A 196  
721 CTGACGGCCTCTTCATGGTCACCACAGCTGTGATCATCAGAGACAAGTATGTGAGGAATG 780  
197 D G L F M V T T A V I I R D K Y V R N V 216  
781 TGTCTGTCTGTCAACAACACCCTGCTCGGCCAGGAGAAGGAAACTGTCATTTTTATTC 840  
217 S C S V N N T L L G Q E K E T V I F I P 236  
841 CAGAATCCTTTATGCCCAGCGCATCTCCCTGGATGGTGGCCCTAGCTGTCATCCTGACCG 900  
237 E S F M P S A S P W M V A L A V I L T A 256  
901 CATCTCCCTGGATGGTGTCCATGACTGTATCCTGGCTGTTTTTCATCATCTTCATGGCTG 960  
257 S P W M V S M T V I L A V F I I F M A V 276

NCBI GeneBank

Figure 7B

961 TCAGCATCTGTTGCATCAAGAACTTCAAAGGGAAAAAAGATTCTGTCAGGGGAAAAGA 1020  
277 S I C C I K K L Q R E K K I L S G E K K 296

1021 AAGTTGAACAAGAGGAAAAAGAAATTGCACAGCAACTTCAAGAAGAATTGCGATGGAGAA 1080  
297 V E Q E E K E I A Q Q L Q E E L R W R R 316

1081 GAACATTCTTACATGCTGCTGATGTGGTCTGGATCCAGACACCGCTCATCCCGAGCTCT 1140  
317 T F L H A A D V V L D P D T A H P E L F 336

1141 TCCTGTCAGAGGACCGGAGAAGTGTGAGGCGGGGCCCTACAGGCAGAGAGTGCCTGACA 1200  
337 L S E D R R S V R R G P Y R Q R V P D N 356

1201 ACCCAGAGAGATTTCGACAGTCAGCCTTGTCTCTGGGATGGGAGAGCTTCGCCTCAGGGA 1260  
357 P E R F D S Q P C V L G W E S F A S G K 376

1261 AACATTACAGGGGAACTTCACAGAGTGGGACCCACCAGAGCCTATAGAATCAATTCTCT 1320  
377 H Y R G N F T E W G P T R A Y R I N S L 396

1321 TGGACTCACAGCCATGCAGAAAGCCCTGGCCATCTCAGCAGCCACCGCACAAACCCCTTA 1380  
397 D S Q P C R K P W P S Q Q P P H N P P N 416

1381 ATGAAAGACACGCCCTCCTCCCCTCTGGTCACGTAAGAGAAACATCTTCCAGCTGCCTTTT 1440  
417 E R H A L L P S G H V R E H L P A A F F 436

1441 TCACACCCACTCCAGCCCTCTGCCCCAGTTTCTCCTCCTCACTAGTCTGTGGCTTTAGT 1500  
437 T P T P A L C P S F L L L T S L W L \* 455

1501 AGTTCCTTTGCTTGTAATTATGGGATGGGATCCAGGCATAGGGAAGTAGTTGTTTCATAG 1560

1561 CTCCCAGTCAAAAAGAAAGTGAGAGAAGCTGTTGGGCAGCGAACCTACTGTTTAAATCA 1620

1621 GGATAACCACATTAAGCCCAATATGCCAGTTGGCACCAGATGCTGTGGACTTGGAATGAG 1680

1681 GCCAACAGGGTTCACCAGGATGAGAGAGGAGAGAGGAATCCACAGGACCACCAGAAGGGA 1740

1741 GAGGGAACCAGATATGCAGATCAGAGATAGAGGAAGTGTGAGAGGAAAGGGGAGGTCCT 1800

1801 GCTGATTCTTCAGAATGGCTTCTGGACCCTGGAGATGTTTGGAACCAATACCGGGCCCT 1860

1861 GTCTCCCCTGAGAGGATTCTCCCTTTGAAGGAGTCCCTTTGCCGGGTGGGCGTCTTCCT 1920

1921 GGACTATGAAGCTGGAGATGTCTCCTTCTACAACATGAGGGACAGATCACACATCTACAC 1980

1981 ATGTCCCCGTTCAGCCTTTAATGTGCCTGTGAGGCCATTCTTCAGGTTAGGGTCTGATGA 2040

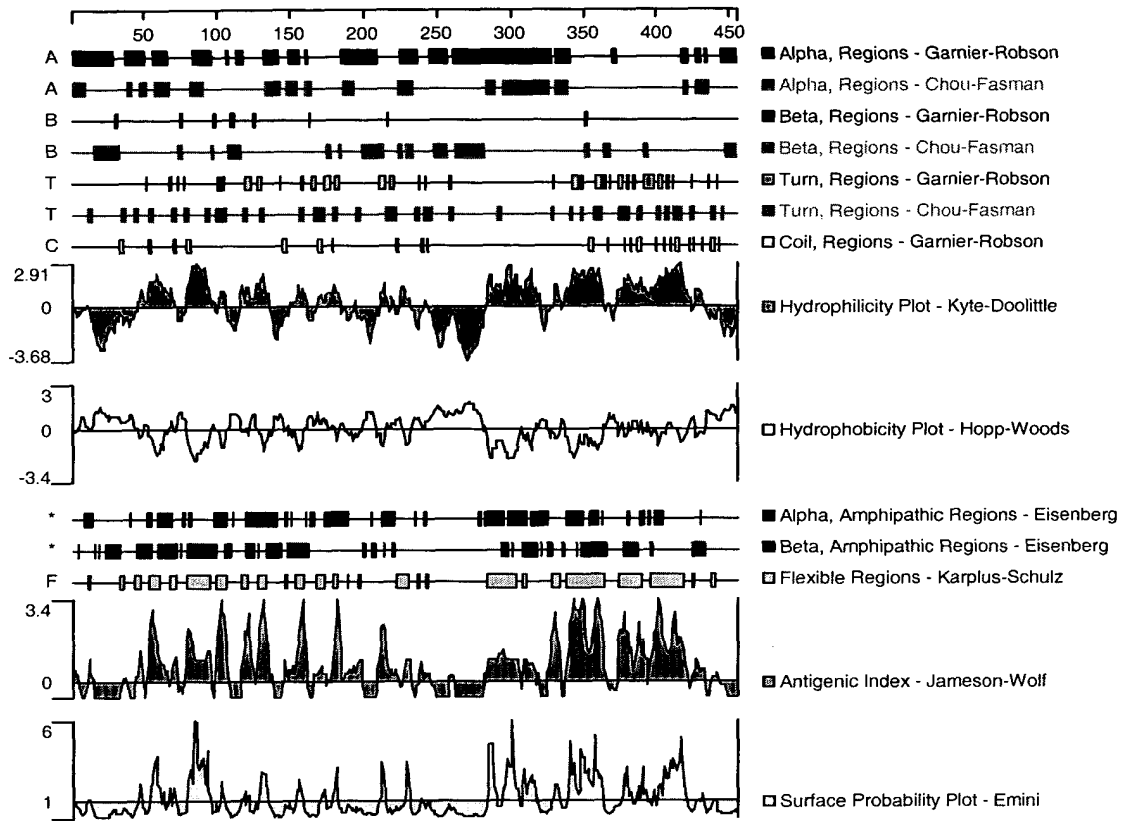
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Figure 7C

2041 CAGCCCCATCTTCATCTGCCCTGCACTCACAGGAGCCAGTGGGGTCATGGTGCCTGAAGA 2100  
2101 GGGCCTGAAACTTCACAGAGTGGGGACCCACCAAGGTTGTAAGGATGGCTAAGTCCCACC 2160  
2161 ATAAGAGCTAAAGGGTCCTGGGAGATGATGGCTCATTTCACCCAACCCAGGATTTCCTCA 2220  
2221 CAGCACACACCCACAGGCCTGGACCTGGGATGAAGATGAATGAAGAACATGGACTCATGT 2280  
2281 GGATGTGGTTTGGCTCAGATGTCCCTGCAATAAACAAGGGGTCAGTACTTAGTCCCTGAG 2340  
2341 TGTGGTTGAGGTTTGAGGTCCTGGTCGAGCAGGGCAGTACTGGACCAGGTCTACGTCAGC 2400  
2401 ATTCAGGTTCAATGGGGACACCAGTGGCTTCAAACCTCCTGATCTAATTATGTTTTTAGA 2460  
2461 CACTTAGAAGTTATTGAGGACTTTAAAGAACTTTTGTTTATTGGGGTTAATATTTATGAC 2520  
2521 ATTTGACCATTGAAACAAAAATTTAAATGTTATCTTTTAATTTATGTTAAAAATAGCATT 2580  
2581 AATAAATCAGTTATAGGTTAATGTAGATAGGATGTTTTGTGAAAAAGCAATCTATTGTGT 2640  
2641 CCAAATAAAAAACAAAAAGTGTAaaaaaaaaaaaaaaaaaaaaa 2682

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Figure 8





[illegible]

1	CGATTCGGCTCCAAACTCCGGCGCTGCAGCCGATCGGACTCTGGGCCCGGTGGGCACCG	60
61	CGCGCAGCTAGGGAGCCGAGAACC GCGCGAGCCCCGAGGACGCCAGAGCGCGAGGGTC	120
121	GCTGCGCCTCGCAGAGCCGGAGCCGAGTCGAGCCGGGCGCCCGGGCTGCCTGGAGACGCC	180
181	GTGACTTTGAAGTGTAACTTCAAGACAGATGGGCGCATGCGGGAGATCGTGTGGTACCGG	240
1	M R E I V W Y R	8
241	GTGACGGATGGTGGCACCATCAAGCAAAAGATCTTCACCTTCGACGCCATGTTCTCCACC	300
9	V T D G G T I K Q K I F T F D A M F S T	28
301	AACTACTCACACATGGAGAACTACCGCAAGCGAGAGGACCTGGTGTACCAGTCCACTGTG	360
29	N Y S H M E N Y R K R E D L V Y Q S T V	48
361	AGGCTGCCCCGAGGTCCGGATCTCAGACAATGGTCCCTATGAGTGCCATGTGGGCATCTAC	420
49	R L P E V R I S D N G P Y E C H V G I Y	68
421	GACCGCGCCACCAGGGAGAAGGTGGTCTTGGCATCAGGCAACATCTTCTCAACGTCATG	480
69	D R A T R E K V V L A S G N I F L N V M	88
481	GCTCCTCCCACCTCCATTGAAGTGGTGGCTGCTGACACACCAGCCCCCTTCAGCCGCTAC	540
89	A P P T S I E V V A A D T P A P F S R Y	108
541	CAAGCCCAGAACTTCACGCTGGTCTGCATCGTGTCTGGAGGAAAACCAGCACCCATGGTT	600
109	Q A Q N F T L V C I V S G G K P A P M V	128
601	TATTTCAAACGAGATGGGGAACCAATCGACGCAGTGCCCCCTATCAGAGCCACCAGCTGCG	660
129	Y F K R D G E P I D A V P L S E P P A A	148
661	AGCTCCGGCCCCCTACAGGACAGCAGGCCCTTCCGCAGCCTTCTGCACCGTGACCTGGAT	720
149	S S G P L Q D S R P F R S L L H R D L D	168
721	GACACCAAGATGCAGAAGTCACTGTCCCTCCTGGACGCCGAGAACCGGGGTGGGCGACCC	780
169	D T K M Q K S L S L L D A E N R G G R P	188
781	TACACGGAGCGCCCCCTCCCGTGGCCTGACCCAGATCCCAACATCCTCCTCCAGCCAACC	840
189	Y T E R P S R G L T P D P N I L L Q P T	208
841	ACAGAGAACATACCAGAGACGGTCGTGAGCCGTGAGTTTCCCCGCTGGGTCCACAGCGCC	900
209	T E N I P E T V V S R E F P R W V H S A	228
901	GAGCCACCTACTTCTCGGCCACAGCCGACCCCCGAGCAGTGACGGCACTGTGGAAGTA	960
229	E P T Y F L R H S R T P S S D G T V E V	248
961	CGTGCCCTGCTCACCTGGACCCTCAACCCACAGATCGACAACGAGGCCCTCTTCAGCTGC	1020
249	R A L L T W T L N P Q I D N E A L F S C	268

Figure 9B

1021 GAGGTCAAGCACCCAGCTCTGTTCGATGCCCATGCAGGCAGAGGTCACGCTGGTTGCCCCC 1080  
269 E V K H P A L S M P M Q A E V T L V A P 288

1081 AAAGGACCCAAAATTGTGATGACGCCCAGCAGAGCCCGGTAGGGGACACAGTGAGGATT 1140  
289 K G P K I V M T P S R A R V G D T V R I 308

1141 CTGGTCCATGGGTTTCAGAACGAAGTCTTCCCGAGCCCATGTTACGTGGACGCGGGTT 1200  
309 L V H G F Q N E V F P E P M F T W T R V 328

1201 GGGAGCCGCTCCTGGACGGCAGCGCTGAGTTCGACGGGAAGGAGCTGGTGTGGAGCGG 1260  
329 G S R L L D G S A E F D G K E L V L E R 348

1261 GTTCCCGCCGAGCTCAATGGCTCCATGTATCGCTGCACCGCCCAGAACCCACTGGGCTCC 1320  
349 V P A E L N G S M Y R C T A Q N P L G S 368

1321 ACCGACACGCACACCCGGCTCATCGTGTGTTGAAAACCCAAATATCCCAAGAGGAACGGAG 1380  
369 T D T H T R L I V F E N P N I P R G T E 388

1381 GACTCTAATGGTTCCATTGGCCCCACTGGTGCCCGGCTCACCTTGGTGCTCGCCCTGACA 1440  
389 D S N G S I G P T G A R L T L V L A L T 408

1441 GTGATTCTGGAGCTGACGTGAAGGCACCCGCCCCGGCCACTCCATCAGGCACTGACATCT 1500  
409 V I L E L T \* 415

1501 CCGCGACCGGTTTTTCATTTCTTTTCTAAACTATTTCCAGTCTTGTTCTTAGTCTCTTTCC 1560

1561 ATCTGTGTCTTGGCTTCTTCAGTCGGTTTAATTAAACAAACAGAACAATTTTCCCCACA 1620

1621 AA 1680

1681 AA 1724

Figure 10

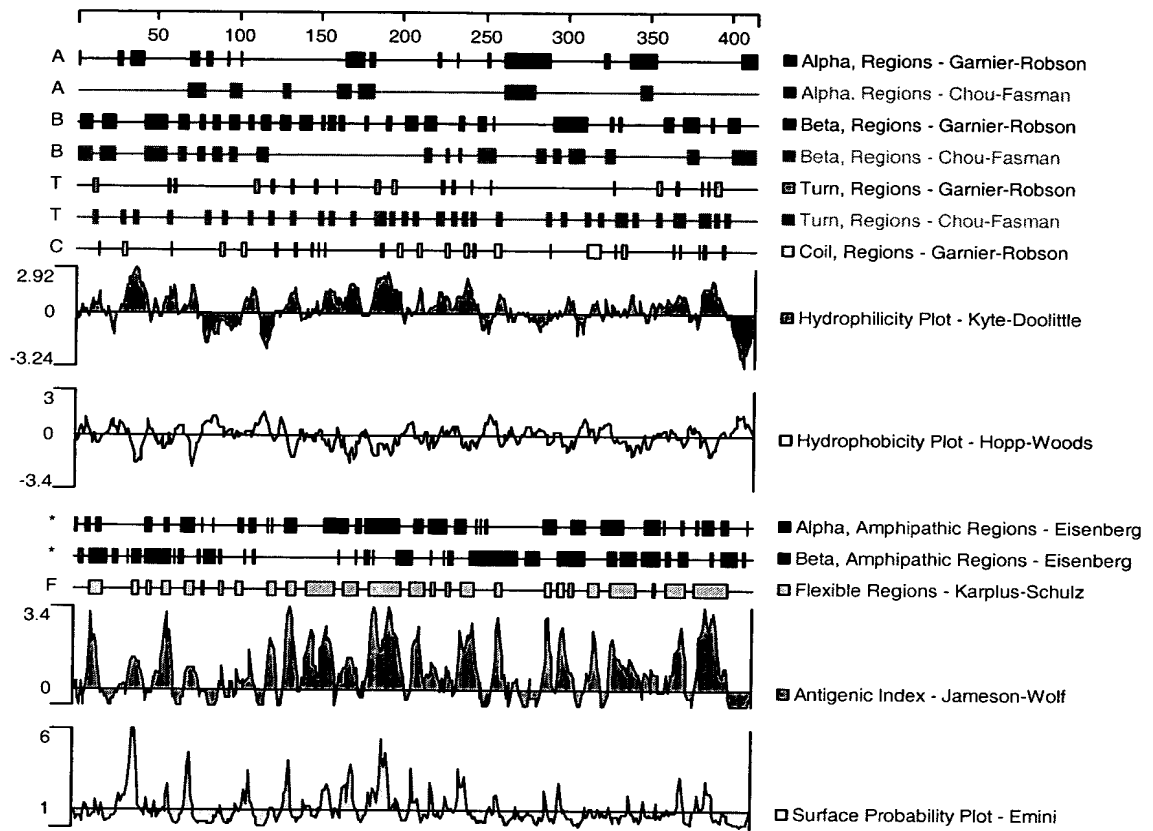


Figure 11

1 CACGAGCCTGTGCCCTGGAAAGGTTGGAGACTTGGGGGACGACTGGAGAATTGCCATTT 60

61 GAGGACCAAAGGAGAAAAGAACTACACGCTAATTCTAGAAGGCCTCCTGTCCCTGCCTG 120

121 CTCTGGGTGCTCATGGAACCAGCTGCTGCCCTGCACTTCTCCCGCCAGCCTCCCTCCTC 180  
1 M E P A A A L H F S R P A S L L 16

181 CTCTCCTCAGCCTGTGTGCACTGGTCTCAGCCCAGGTCACTGTGCGTGGGGCCCACTGAT 240  
17 L L L S L C A L V S A Q V T V V G P T D 36

241 CCCATCCTGGCCATGGTGGGAGAAAACACTACGTTACGATGCTGTCTGTCAACCCGAGGAA 300  
37 P I L A M V G E N T T L R C C L S P E E 56

301 AATGCTGAGGACATGGAGGTGCGGTGGTTCAGTCTCAGTTCTCCCCTGCAGTGTGTTGTG 360  
57 N A E D M E V R W F Q S Q F S P A V F V 76

361 TATAAGGGTGAAGAGAGAGAACAGAGGAGCAGAAGGAGGAGTACCGAGGGAGAACCACC 420  
77 Y K G G R E R T E E Q K E E Y R G R T T 96

421 TTTGTGAGCAAAGACAGCAGGGGAGCGTGGCCCTGATCATAACAATGTACAGCCGAG 480  
97 F V S K D S R G S V A L I I H N V T A E 116

481 GATAACGGCATCTACCACTGTTACTTCCAAGAAGGCAGGTCTTGCAATGAGGCCATCCTG 540  
117 D N G I Y Q C Y F Q E G R S C N E A I L 136

541 CACCTTGTGGTGGCAGACCAGCACAATCCTCTTTCTGGATCCCCATTCCGCAGGGGACA 600  
137 H L V V A D Q H N P L S W I P I P Q G T 156

601 CTCTCCCTATGAAAAGAAGATTCCAGGGGAAAAATCCTTCCTCCTGCACAAGGGCCACCA 660  
157 L S L \* 160

661 TGAGTGAGTTTGCCCTGCTAAGCCGTGGGCTTGACTTCTTGAGAAGCACATGCAGAACTC 720

721 AGTTGAGGCCATGAGCCGGGGGAAAATGGTGAATCTCGGAAGAGAAGTCCTATGCCTGCC 780

781 TTAGCACTGAGCTGTGCACTTCTGAGAGTGAGAGGAGACACCATCAATAATTGTCTTGGG 840

841 ACAACTGGAATAAACAGTGACTGCCCAGAGAACTACGATATTTGAAATCTTATTTCTTGA 900

901 TGAATATTCATCCTGACTTCTTTCTGAAATGCTGTTTGCAAAGAGAGTGACTTATATGT 960

961 AAGTAGAGCGTTTTATTAAAGCAAGACTTAATACAGAAGCAAAAAAAAAAAAAAAAAAAAA 1019

Figure 12

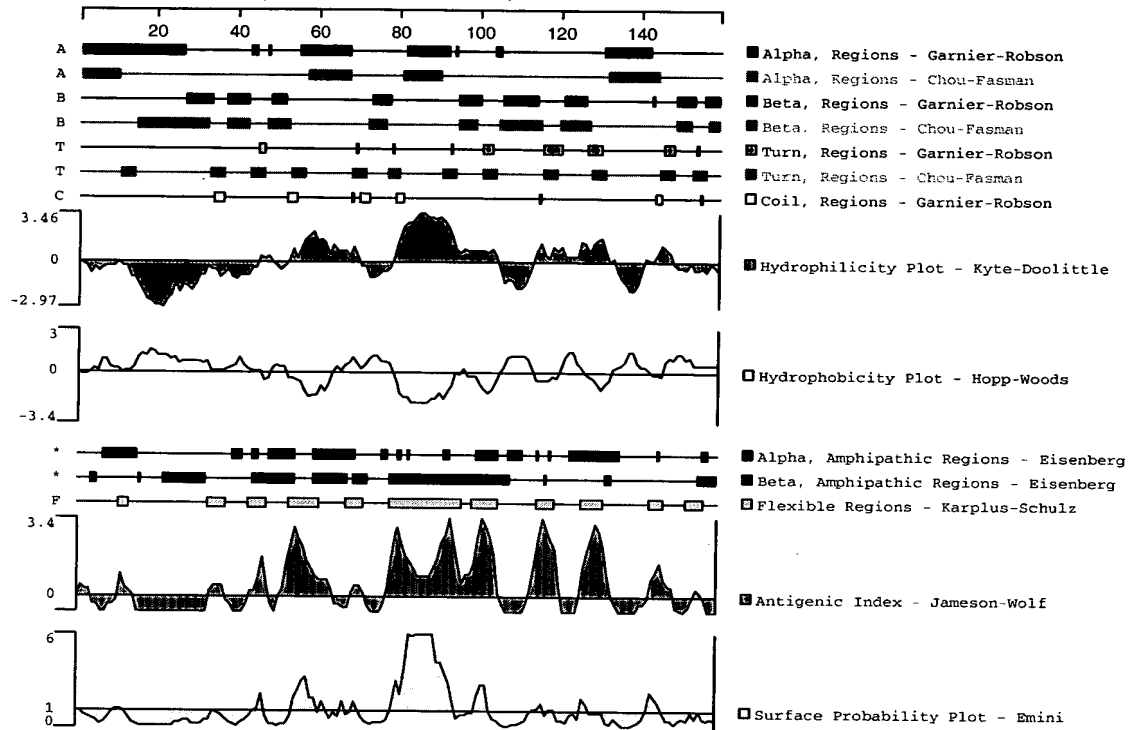


Figure 13A

1 ACATCCATGGCTCTAATGCTCAGTTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAG 60  
1 M A L M L S L V L S L L K L G S G Q 18

61 TGGCAGGTGTTTGGGCCAGACAAGCCTGTCCAGGCCCTGGTGGGGAGGACGCAGCATTC 120  
19 W Q V F G P D K P V Q A L V G E D A A F 38

121 TCCTGTTTCTGTCTCCTAAGACCAATGCAGAGGCCATGGAAGTGGGTTCTTCAGGGGC 180  
39 S C F L S P K T N A E A M E V R F F R G 58

181 CAGTTCTCTAGCGTGGTCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATG 240  
59 Q F S S V V H L Y R D G K D Q P F M Q M 78

241 CCACAGTATCAAGGCAGGACAAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCT 300  
79 P Q Y Q G R T K L V K D S I A E G R I S 98

301 CTGAGGCTGGAACATTACTGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCC 360  
99 L R L E N I T V L D A G L Y G C R I S S 118

361 CAGTCTTACTACCAGAAGGCCATCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCTT 420  
119 Q S Y Y Q K A I W E L Q V S A L G S V P 138

421 CTCATTTCCATCACGGGATATGTTGATAGAGACATCCAGCTACTCTGTCTCAGTCTCGGGC 480  
139 L I S I T G Y V D R D I Q L L C Q S S G 158

481 TGGTTCCTCCGGCCACAGCGAAGTGGAAAGGTCCACAAGGACAGGATTTGTCCACAGAC 540  
159 W F P R P T A K W K G P Q G Q D L S T D 178

541 TCCAGGACAAACAGAGACATGCATGGCCTGTTTGTGATGTGGAGATCTCTCTGACCGTCCAA 600  
179 S R T N R D M H G L F D V E I S L T V Q 198

601 GAGAACGCCGGGAGCATATCCTGTTCCATGCGGCATGCTCATCTGAGCCGAGAGGTGGAA 660  
199 E N A G S I S C S M R H A H L S R E V E 218

661 TCCAGGGTACAGATAGGAGATACCTTTTTCGAGCCTATATCGTGGCACCTGGCTACCAAA 720  
219 S R V Q I G D T F F E P I S W H L A T K 238

721 G TACTGGGAATACTCTGCTGTGGCCTATTTTTTGGCATGTGTTGACTGAAGATTTTCTTC 780  
239 V L G I L C C G L F F G I V G L K I F F 258

781 TCCAAATTCCAGTGGAATCCAGGCGAACTGGACTGGAGAAGAAAGCACGGACAGGCA 840  
259 S K F Q W K I Q A E L D W R R K H G Q A 278

841 GAATTGAGAGACGCCCCGAAACACGCAGTGGAGGTGACTCTGGATCCAGAGACGGCTCAC 900  
279 E L R D A R K H A V E V T L D P E T A H 298

901 CCGAAGCTCTGCGTTTCTGATCTGAAAACGTAAACCCATAGAAAAGCTCCCCAGGAGGTG 960  
299 P K L C V S D L K T V T H R K A P Q E V 318

Figure 13B

961 CCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCTTCTCAGAGTTTCCAAGCA 1020  
319 P H S E K R F T R K S V V A S Q S F Q A 338

1021 GGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAAAGGTGGCGGTGGGAGTGTGC 1080  
339 G K H Y W E V D G G H N K R W R V G V C 358

1081 CGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCGATCATGGGTACTGG 1140  
359 R D D V D R R K E Y V T L S P D H G Y W 378

1141 GTCCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGTTTTATCAGCGTC 1200  
379 V L R L N G E H L Y F T L N P R F I S V 398

1201 TTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCCTGGACTATGAGTGTGGGACCATC 1260  
399 F P R T P P T K I G V F L D Y E C G T I 418

1261 TCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCCTGACATGTCGGTTTGAAGGC 1320  
419 S F F N I N D Q S L I Y T L T C R F E G 438

1321 TTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCCAGAGAC 1380  
439 L L R P Y I E Y P S Y N E Q N G T P R D 458

1381 AAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTTCCTCCCCAGGGGTGAAATGTA 1440  
459 K Q Q \* 462

1441 GGATGAATCACATCCCACATTCTTCTTTAGGGATATTAAGGTCTCTCTCCAGATCCAAA 1500

1501 GTCCCGCAGCAGCCGCCAAGGTGGCTTCCAGATGAAGGGGGACTGGCCTGTCCACATGG 1560

1561 GAGTCAGGTGTCATGGCTGCCCTGAGCTGGGAGGGAAGAAGGCTGACATTACATTTAGTT 1620

1621 TGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCGTC 1680

1681 AGGAATTCCCATCTCACAGGCTGTGGTGTAGATTAAGTAGACAAGGAATGTGAATAATGC 1740

1741 TTAGATCTTATTGATGACAGAGTGATCCTAATGGTTGTTTCATTATATTACACTTTCAG 1800

1801 TAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1833

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Figure 14

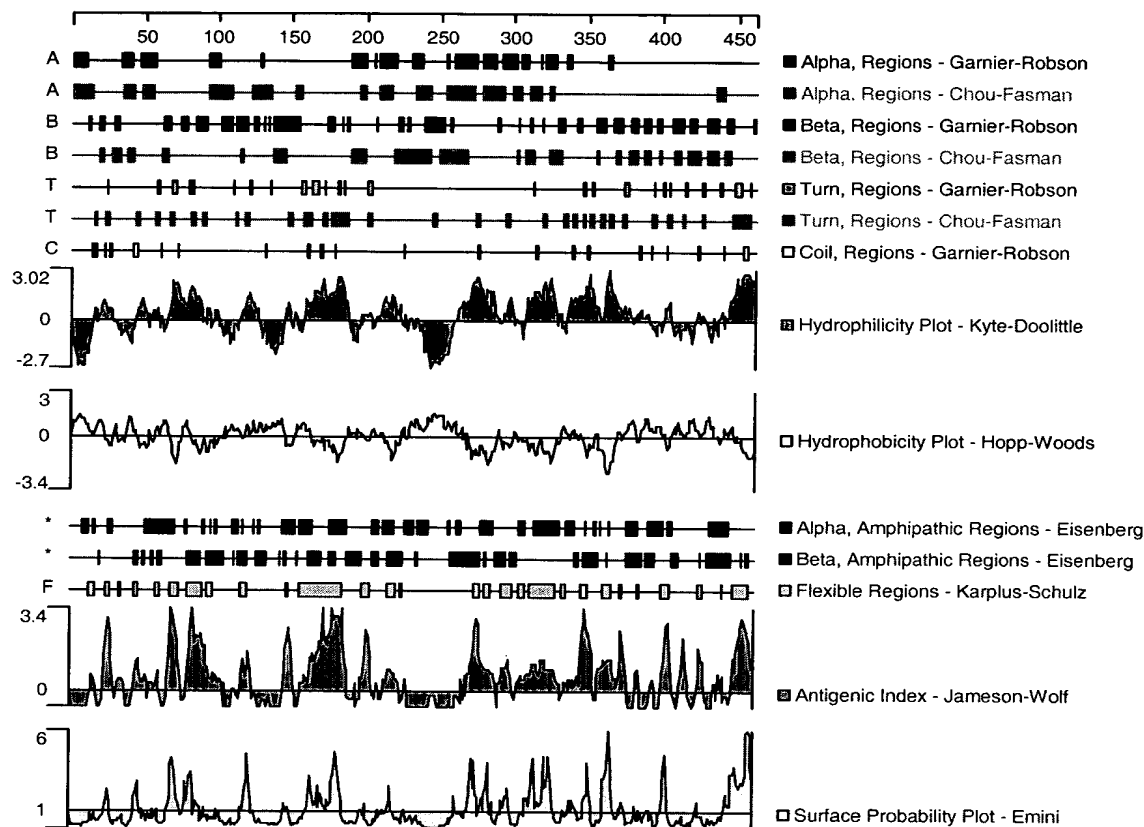




Figure 15

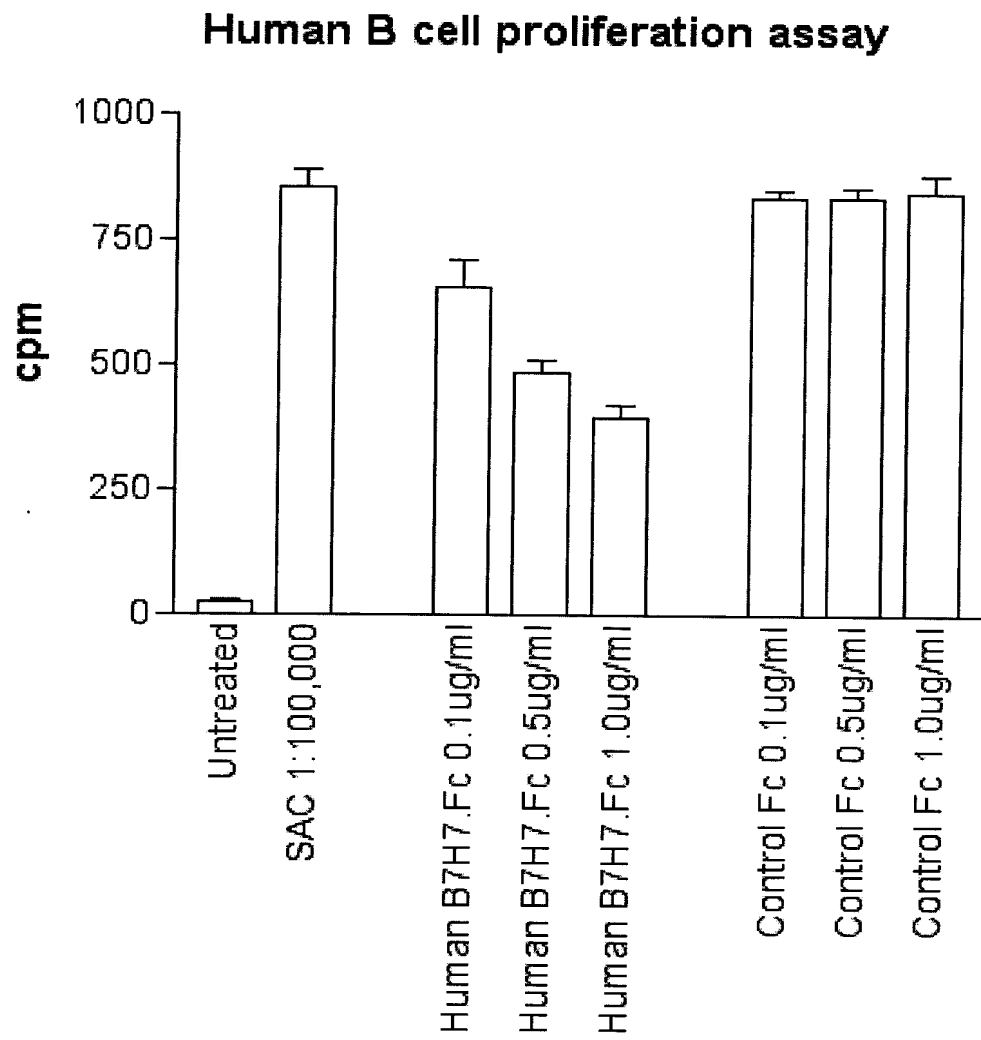


Figure 16

